

WHAT IS CLAIMED IS:

1. An isolated or recombinant polypeptide comprising a sequence having at least 97% amino acid sequence identity to any one of SEQ ID NO: 75 to SEQ ID NO: 108.

2. The polypeptide of claim 1, wherein said polypeptide comprises lipase activity.

3. The polypeptide of claim 1, wherein said polypeptide degrades geranyl butyrate, neryl butyrate, or both geranyl butyrate and neryl butyrate.

4. The polypeptide of claim 3, wherein said polypeptide exhibits enantioselectivity for geranyl butyrate over neryl butyrate.

5. The polypeptide of claim 4, comprising a sequence selected from: SEQ ID NO:76, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:86, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:78, SEQ ID NO:87, SEQ ID NO:100, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:88, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:103, or SEQ ID NO:106.

6. The polypeptide of claim 3, wherein said polypeptide exhibits enantioselectivity for neryl butyrate over geranyl butyrate.

7. The polypeptide of claim 6, comprising a sequence selected from: SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:105, SEQ ID NO:84, SEQ ID NO:91, SEQ ID NO:92, or SEQ ID NO:93.

8. The polypeptide of claim 1, comprising a polypeptide encoded by a polynucleotide sequence, which polynucleotide sequence hybridizes under highly stringent conditions over substantially the entire length of: a polynucleotide sequence selected from SEQ ID NO: 1 to SEQ ID NO: 54, or a complementary sequence thereof; or a polynucleotide sequence encoding a polypeptide sequence selected from SEQ ID NO: 55 to SEQ ID NO: 108, or a complementary sequence thereof; wherein said polypeptide comprises one or more

of: Lys at position 1; Thr at position 14; Ser at position 17; Arg at position 22; Glu at position 26; Pro at position 31; Gly at position 33; Glu at position 34; Pro at position 35; Pro or Thr at position 37; Ser or Lys at position 41; Gly at position 42; Arg or Glu at position 43; Ala at position 61; Tyr at position 75; Gly at position 96; Ser at position 97; Thr at position 104; Ser at position 107; Ala at position 125; Gly at position 129; Val at position 134; Cys at position 138; Lys at position 141; Lys at position 146; Thr at position 156; Met at position 160; Arg at position 166; or His at position 177.

9. The polypeptide of claim 1 comprising one or more of: Lys at position 1; Thr at position 14; Ser at position 17; Arg at position 22; Glu at position 26; Pro at position 31; Gly at position 33; Glu at position 34; Pro at position 35; Pro or Thr at position 37; Ser or Lys at position 41; Gly at position 42; Arg or Glu at position 43; Ala at position 61; Tyr at position 75; Gly at position 96; Ser at position 97; Thr at position 104; Ser at position 107; Ala at position 125; Gly at position 129; Val at position 134; Cys at position 138; Lys at position 141; Lys at position 146; Thr at position 156; Met at position 160; Arg at position 166; or His at position 177.

10. The polypeptide of claim 9, wherein said polypeptide has lipase activity.

11. The polypeptide of claim 9, wherein said polypeptide degrades geranyl butyrate, neryl butyrate, or both geranyl butyrate and neryl butyrate.

12. The polypeptide of claim 11, wherein said polypeptide exhibits enantioselectivity for geranyl butyrate over neryl butyrate.

13. The polypeptide of claim 12, comprising one or more of: Arg at position 22; Gly at position 33; Ser or Lys at position 41; Arg at position 43; Ser at position 107; Lys at position 141; Lys at position 146; Met at position 160; or His at position 177.

14. The polypeptide of claim 12, comprising one or more of: Arg at position 43; or Ser at position 107.

15. The polypeptide of claim 11, wherein said polypeptide exhibits enantioselectivity for neryl butyrate over geranyl butyrate.

16. The polypeptide of claim 15, comprising one or more of: Ser at position 17; Arg at position 22; Pro at position 31; Gly at position 33; Ser or Lys at position 41; Lys at position 141; Lys at position 146; Met at position 160; Arg at position 166; or His at position 177.

17. The polypeptide of claim 15, comprising one or more of: Ser at position 17; Pro at position 31; or Arg at position 166.

18. An isolated or recombinant polypeptide comprising a sequence having at least 94% amino acid sequence identity to the mature region of SEQ ID NO: 55, 61, 64, 65, 67, 68, 70 or 72.

19. The polypeptide of claim 18, wherein said polypeptide comprises a sequence having at least 94% amino acid sequence identity to the mature region of SEQ ID NO: 55.

20. The polypeptide of claim 19, wherein said polypeptide comprises a sequence selected from SEQ ID NO: 55, 58-62, 75-78, 80-88, or 94-108, or the mature region thereof.

21. The polypeptide of claim 18, wherein said polypeptide comprises a sequence having at least 94% amino acid sequence identity to the mature region of SEQ ID NO: 61.

22. The polypeptide of claim 21, wherein said polypeptide comprises a sequence selected from SEQ ID NO: 55, 57-62, 75-78, 80-90, or 93-108, or the mature region thereof.

23. The polypeptide of claim 18, wherein said polypeptide comprises a sequence having at least 94% amino acid sequence identity to the mature region of SEQ ID NO: 64.

24. The polypeptide of claim 23, wherein said polypeptide comprises a sequence selected from SEQ ID NO: 64, 71, or 72, or the mature region thereof.

25. The polypeptide of claim 18, wherein said polypeptide comprises a sequence having at least 94% amino acid sequence identity to the mature region of SEQ ID NO: 65.

26. The polypeptide of claim 25, wherein said polypeptide comprises a sequence selected from SEQ ID NO: 65, 66, or 73, or the mature region thereof.

27. The polypeptide of claim 18, wherein said polypeptide comprises a sequence having at least 94% amino acid sequence identity to the mature region of SEQ ID NO: 67.

28. The polypeptide of claim 27, wherein said polypeptide comprises the sequence SEQ ID NO: 67, or the mature region thereof.

29. The polypeptide of claim 18, wherein said polypeptide comprises a sequence having at least 94% amino acid sequence identity to the mature region of SEQ ID NO: 68.

30. The polypeptide of claim 29, wherein said polypeptide comprises a sequence selected from SEQ ID NO: 68 or 101, or the mature region thereof.

31. The polypeptide of claim 18, wherein said polypeptide comprises a sequence having at least 94% amino acid sequence identity to the mature region of SEQ ID NO: 70.

32. The polypeptide of claim 31, wherein said polypeptide comprises a sequence selected from SEQ ID NO: 63, 68-70, 82-83, 85-86, 96, or 101-102, or the mature region thereof.

33. The polypeptide of claim 18, wherein said polypeptide comprises a sequence having at least 94% amino acid sequence identity to the mature region of SEQ ID NO: 72.

34. The polypeptide of claim 33, wherein said polypeptide comprises a sequence selected from SEQ ID NO: 64, 71, or 72, or the mature region thereof.

35. An isolated or recombinant polypeptide comprising a sequence having at least 85% amino acid sequence identity to the mature region of SEQ ID NO: 74.

36. The polypeptide of claim 35, wherein said polypeptide comprises a sequence selected from SEQ ID NO: 63, 71-72, 74, or 79.

5 37. An isolated or recombinant polypeptide comprising a sequence having at least 99% amino acid sequence identity to the mature region of SEQ ID NO: 56.

38. An isolated or recombinant polypeptide exhibiting enantioselective lipase activity, which polypeptide comprises an amino acid sequence of any one of SEQ ID NO: 55 through SEQ ID NO: 108.

10 39. An isolated or recombinant polypeptide exhibiting enantioselective lipase activity, which polypeptide comprises at least 45 contiguous amino acid residues of a polypeptide encoded by a coding polynucleotide sequence, the coding polynucleotide sequence selected from the group consisting of:

15 (a) a polynucleotide sequence selected from any of SEQ ID NO: 1 to SEQ ID NO: 54;

(b) a polynucleotide sequence that encodes a polypeptide selected from any of SEQ ID NO: 55 to SEQ ID NO: 108; and,

20 (c) a polynucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a polynucleotide sequence (a) or (b), or which hybridizes to a subsequence comprising at least 100 nucleotides thereof, wherein the polynucleotide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, 25 AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064,

CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340,
E01903, E02083, E05047, JW0068, M74010, P37957, S23934,
U78785, X95309, Z99105, and Z99108.

5 **40.** The isolated or recombinant polypeptide of claim 38, wherein the
polypeptide is enantioselective for either a *cis* form substrate enantiomer or for a *trans* form
substrate enantiomer.

41. The isolated or recombinant polypeptide of claim 40, wherein the
polypeptide comprises an enantiomeric ratio of at least 2 for the *cis* form substrate
enantiomer or for the *trans* form substrate enantiomer.

10 **42.** The isolated or recombinant polypeptide of claim 40, wherein the
polypeptide comprises an enantiomeric ratio of at least 5 for the *cis* form substrate
enantiomer or for the *trans* form substrate enantiomer.

15 **43.** The isolated or recombinant polypeptide of claim 40, wherein the
polypeptide comprises an enantiomeric ratio of at least 10 for the *cis* form substrate
enantiomer or for the *trans* form substrate enantiomer.

44. The isolated or recombinant polypeptide of claim 40, wherein the
polypeptide comprises an enantiomeric ratio of at least 50 for the *cis* form substrate
enantiomer or for the *trans* form substrate enantiomer.

20 **45.** The isolated or recombinant polypeptide of claim 40, wherein the
polypeptide comprises an enantiomeric ratio of at least 100 for the *cis* form substrate
enantiomer or for the *trans* form substrate enantiomer.

46. An isolated or recombinant polypeptide which is at least 99% or more
identical over a comparison window of 45 contiguous amino acids to one or more of SEQ ID
NO: 55 to SEQ ID NO: 108.

25 **47.** An isolated or recombinant polypeptide encoded by a nucleic acid
comprising a polynucleotide sequence selected from the group consisting of:

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(a) a polynucleotide sequence selected from SEQ ID NO: 1 to SEQ ID NO: 54, or a complementary polynucleotide sequence thereof;

(b) a polynucleotide sequence encoding a polypeptide selected from SEQ ID NO: 55 to SEQ ID NO: 108, or a complementary polynucleotide sequence thereof;

(c) a polynucleotide sequence which hybridizes under highly stringent conditions over substantially the entire length of polynucleotide sequence (a) or (b), or which hybridizes to a subsequence thereof comprising at least 100 residues thereof, wherein the polynucleotide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108;

(d) a polynucleotide sequence comprising all or a fragment of (a), (b), or (c), wherein the fragment encodes a polypeptide comprising lipase activity; and,

(e) a polynucleotide sequence encoding a polypeptide, the polypeptide comprising an amino acid sequence which is substantially identical over at least 45 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623,

AJ297356, BAA11406, BAA22231, BAB05967, C69652,
CAA00273, CAA00274, CAA02196, CAA64621, CAB12064,
CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340,
E01903, E02083, E05047, JW0068, M74010, P37957, S23934,
U78785, X95309, Z99105, and Z99108.

5 **48.** A polynucleotide sequence encoding a polypeptide comprising lipase activity produced by mutating or recombining one or more polynucleotide sequence of claim 47.

10 **49.** The isolated or recombinant polypeptide of claim 47, the polypeptide comprising an amino acid sequence of any one of SEQ ID NO: 55 to SEQ ID NO: 108.

15 **50.** The isolated or recombinant polypeptide of claim 47, wherein the encoded polypeptide exhibits lipase activity.

51. The isolated or recombinant polypeptide of claim 50, wherein the encoded polypeptide exhibits enantioselective lipase activity.

20 **52.** The isolated or recombinant polypeptide of claim 50, wherein the encoded polypeptide exhibits lipase activity with respect to tributyrin.

53. The isolated or recombinant polypeptide of claim 50, wherein the encoded polypeptide exhibits lipase activity with respect to tributyrin in DMF.

25 **54.** The isolated or recombinant polypeptide of claim 50, wherein the encoded polypeptide exhibits lipase activity with respect to tributyrin after heat treatment.

55. The isolated or recombinant polypeptide of claim 50, wherein the encoded polypeptide exhibits enantioselective lipase activity with respect to neryl- butyrate.

56. The isolated or recombinant polypeptide of claim 50, wherein the encoded polypeptide exhibits enantioselective lipase activity with respect to geranyl- butyrate.

57. The isolated or recombinant polypeptide of claim 50, wherein the encoded polypeptide exhibits lipase activity with respect to methyl esters.

58. The isolated or recombinant polypeptide of claim 50, wherein the encoded polypeptide exhibits lipase activity with respect to pentadecanolide.

5 59. The isolated or recombinant polypeptide of claim 50, wherein the encoded polypeptide exhibits lipase activity with respect to oxacyclotridecan.

60. An isolated or recombinant polypeptide comprising at least 45 contiguous amino acid residues of any of the polypeptides of claim 47, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank
10 accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957,
15 S23934, U78785, X95309, Z99105, and Z99108.

61. The isolated or recombinant polypeptide of claim 60, which is substantially identical over at least 50 contiguous amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574,
20 AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

25 62. The isolated or recombinant polypeptide of claim 61, which is substantially identical over at least 75 contiguous amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840,

AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

5 **63.** The isolated or recombinant polypeptide of claim 62, which is substantially identical over at least 100 contiguous amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840,
10 AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

64. The isolated or recombinant polypeptide of claim 63, which is
15 substantially identical over at least 125 contiguous amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652,
20 CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

65. The isolated or recombinant polypeptide of claim 64, which is
25 substantially identical over at least 150 contiguous amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971,
30 CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

66. The isolated or recombinant polypeptide of claim 65, which is substantially identical over at least 175 contiguous amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

67. The isolated or recombinant polypeptide of claim 66, which is substantially identical over at least 180 contiguous amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

68. The isolated or recombinant polypeptide of claim 67, which is substantially identical over at least 200 contiguous amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

69. The isolated or recombinant polypeptide of claim 68, which is substantially identical over at least 212 amino acids of the encoded polypeptide, wherein the

polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

70. The isolated or recombinant polypeptide of claim 69, which is substantially identical over at least 213 amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

71. The isolated or recombinant polypeptide of claim 70, which is substantially identical over at least 215 amino acids of the encoded polypeptide, wherein the polypeptide sequence does not comprise a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

72. The polypeptide of claim 1, 18, 35, 36, or 47, comprising a leader sequence.

73. The polypeptide of claim 1, 18, 35, 36, or 47, comprising a precursor polypeptide.

74. The polypeptide of claim 1, 18, 35, 36, or 47, wherein the polypeptide comprises a secretion signal or a localization signal.

75. The polypeptide of claim 1, 18, 35, 36, or 47, wherein the polypeptide comprises an epitope tag.

5 76. The polypeptide of claim 1, 18, 35, 36, or 47, wherein the polypeptide comprises a fusion protein comprising one or more additional amino acid sequences.

77. The polypeptide of claim 1, 18, 35, 36, or 47, further comprising a polypeptide purification subsequence.

10 78. The polypeptide of claim 77, wherein the polypeptide purification subsequence is selected from the group consisting of: an epitope tag, a FLAG tag, a polyhistidine sequence, and a GST fusion.

79. The polypeptide of claim 1, 18, 35, 36, or 47, further comprising a methionine residue at the N-terminus.

15 80. The polypeptide of claim 1, 18, 35, 36, or 47, wherein the polypeptide further comprises a modified amino acid.

81. The polypeptide of claim 80, wherein the modified amino acid is selected from the group consisting of: a glycosylated amino acid, a PEGylated amino acid, a farnesylated amino acid, an acetylated amino acid, a biotinylated amino acid, an amino acid conjugated to a lipid moiety, and an amino acid conjugated to an organic derivatizing agent.

20 82. A composition comprising one or more polypeptide of claim 80 and a pharmaceutically acceptable excipient.

83. A composition comprising one or more polypeptide of claim 1, 18, 35, 36, or 47, and a pharmaceutically acceptable excipient.

25 84. A polypeptide which comprises a unique subsequence in a polypeptide selected from SEQ ID NO: 55 to SEQ ID NO: 108, wherein the unique subsequence is

unique as compared to a polypeptide sequence corresponding to an amino acid sequence or encoded by a nucleic acid sequence corresponding to any of GenBank accession numbers:

1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257,
AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623,
5 AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274,
CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850,
D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785,
X95309, Z99105, and Z99108.

85. A polypeptide which is specifically bound by a polyclonal antisera raised
10 against at least one antigen, which at least one antigen comprises at least one amino acid
sequence of SEQ ID NO: 55 to SEQ ID NO: 108, or a fragment thereof, wherein the antisera
is subtracted with a polypeptide sequence corresponding to an amino acid sequence or
encoded by a nucleic acid sequence corresponding to any of GenBank accession numbers:

1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257,
15 AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623,
AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274,
CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850,
D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785,
X95309, Z99105, and Z99108.

86. An antibody or antisera produced by administering the polypeptide of
20 claim 1, 18, 35, 36, or 47 to a mammal, which antibody or antisera specifically binds at least
one antigen, said at least one antigen comprising a polypeptide comprising any one of the
amino acid sequences of SEQ ID NO: 55 to SEQ ID NO: 108, which antibody or antisera
does not specifically bind to a peptide encoded by a nucleic acid corresponding to one or

25 more of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992,
AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617,
AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967,
C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664,
CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068,
30 M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

87. An antibody or antisera which specifically binds a polypeptide, the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the antibody does not specifically bind to a peptide encoded by a nucleic acid corresponding to one or more of GenBank accession numbers:

5 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785,
10 X95309, Z99105, and Z99108.

88. An isolated or recombinant nucleic acid comprising: a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence selected from SEQ ID NO: 1 to SEQ ID NO: 54, or a complementary polynucleotide sequence thereof;

15 (b) a polynucleotide sequence encoding a polypeptide selected from SEQ ID NO: 55 to SEQ ID NO: 108, or a complementary polynucleotide sequence thereof;

20 (c) a polynucleotide sequence which hybridizes under highly stringent conditions over substantially the entire length of polynucleotide sequence (a) or (b), or which hybridizes to a subsequence thereof comprising at least 100 residues, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850,
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D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108; and,

(d) a polynucleotide sequence comprising all or a fragment of (a), (b), or (c), wherein the fragment encodes a polypeptide comprising lipase activity, and wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

89. An isolated or recombinant nucleic acid comprising a polynucleotide sequence encoding a polypeptide, the polypeptide comprising an amino acid sequence which is substantially identical over at least 45 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

90. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 45 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding

to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

91. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 50 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

92. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 75 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

93. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 100 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108,

wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

94. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 125 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

95. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 150 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

96. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least

175 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

97. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 200 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

98. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 180 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

99. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 212 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

100. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 213 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

101. The isolated or recombinant nucleic acid of claim 89, wherein the polypeptide comprises an amino acid sequence which is substantially identical over at least 215 contiguous amino acid residues of any one of SEQ ID NO: 55 to SEQ ID NO: 108, wherein the polynucleotide subsequence is unique as compared to a sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

102. The nucleic acid of claim 88 or 89, wherein the encoded polypeptide exhibits lipase activity.

103. The nucleic acid of claim 88 or 89, wherein the encoded polypeptide exhibits enantioselective lipase activity.

5 **104.** The nucleic acid of claim 102, wherein the encoded polypeptide exhibits lipase activity with respect to tributyrin.

105. The nucleic acid of claim 102, wherein the encoded polypeptide exhibits lipase activity with respect to tributyrin in DMF.

10 **106.** The nucleic acid of claim 102, wherein the encoded polypeptide exhibits lipase activity with respect to tributyrin after heat treatment.

107. The nucleic acid of claim 103, wherein the encoded polypeptide exhibits enantioselective lipase activity with respect against neryl-butyrate.

108. The nucleic acid of claim 103, wherein the encoded polypeptide exhibits enantioselective lipase activity with respect to geranyl-butyrate.

15 **109.** The nucleic acid of claim 102, wherein the encoded polypeptide exhibits lipase activity with respect to methyl esters.

110. The nucleic acid of claim 102, wherein the encoded polypeptide exhibits lipase activity with respect to pentadecanolide.

20 **111.** The nucleic acid of claim 102, wherein the encoded polypeptide exhibits lipase activity with respect to oxacyclotridecan.

112. An isolated or recombinant nucleic acid comprising a polynucleotide sequence encoding a polypeptide comprising lipase activity produced by mutating or recombining one or more polynucleotide sequence of claim 88.

25 **113.** The nucleic acid of claim 112, wherein the encoded polypeptide comprises enantioselective lipase activity.

114. The nucleic acid of claim 88, 89, or 112, wherein the encoded polypeptide comprises a leader sequence.

115. The nucleic acid of claim 88, 89, or 112, wherein the encoded polypeptide comprises a precursor peptide.

5 **116.** The nucleic acid of claim 88, 89, or 112, wherein the encoded polypeptide comprises an epitope tag sequence.

117. The nucleic acid of claim 88, 89, or 112, wherein the nucleic acid encodes a fusion protein, said nucleic acid comprising one or more additional nucleic acid sequences.

10 **118.** A composition comprising two or more nucleic acids of claim 88, 89, or 112.

119. A composition of claim 118, wherein the composition comprises a library comprising at least about 2, 5, 10, 50, or more of the nucleic acids.

15 **120.** A composition produced by cleaving of one or more nucleic acid of claim 88, 89, or 112.

121. The composition of claim 120, wherein the cleaving comprises mechanical, chemical or enzymatic cleavage.

122. The composition of claim 121, wherein the enzymatic cleavage comprises cleavage with a restriction endonuclease, an RNase or a DNase.

20 **123.** A composition produced by a process comprising incubating one or more nucleic acids of claim 88, 89, or 112, in the presence of deoxyribonucleotide triphosphates and a nucleic acid polymerase.

124. The composition of claim 123, wherein the nucleic acid polymerase is a thermostable polymerase.

125. A cell comprising at least one nucleic acid of claim 88, 89, or 112, or a cleaved or amplified fragment or product thereof.

126. The cell of claim 125, wherein the cell expresses a polypeptide encoded by the nucleic acid.

5 **127.** A vector comprising the nucleic acid of claim 88, 89, or 112.

128. The vector of claim 127, wherein the vector comprises a plasmid, a cosmid, a phage, a virus or a fragment of a virus.

129. The vector of claim 127, wherein the vector comprises an expression vector.

10 **130.** A cell transduced by the vector of claim 127.

131. A composition comprising a polypeptide encoded by a nucleic acid selected from the nucleic acids of claim 88, 89, or 112, and an excipient.

132. The composition of claim 131, wherein the excipient is a pharmaceutically acceptable excipient.

15 **133.** A composition comprising a polypeptide of claim 88, 89, or 112, wherein the composition comprises a cleaning solution.

134. The composition of claim 133, wherein the cleaning solution further comprises one or more of: a builder, a surfactant, a polymer, a bleach system, a structurant, a pH adjuster, a humectant, or a neutral inorganic salt.

20 **135.** A nucleic acid which comprises a unique subsequence in a nucleic acid selected from SEQ ID NO: 1 to SEQ ID NO: 54, wherein the unique subsequence is unique as compared to a nucleic acid sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623,
25 AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274,

CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

136. A target nucleic acid which hybridizes under stringent conditions to a unique coding oligonucleotide which encodes a unique subsequence in a polypeptide selected from SEQ ID NO: 55 to SEQ ID NO: 108, wherein the unique subsequence is unique as compared to an amino acid sequence or to a polypeptide encoded by a nucleic acid sequence corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108.

137. The nucleic acid of claim 136, wherein the stringent conditions are selected such that a perfectly complementary oligonucleotide to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least a 5x higher signal to noise ratio than for hybridization of the perfectly complementary oligonucleotide to a control nucleic acid corresponding to any of GenBank accession numbers: 1I6WA, 1I6WB, A02813, A02815, A34992, AAA22574, AAB31769, AAC12257, AAD30278, AAF40217, AAF63229, AB000617, AF134840, AF141874, AF237623, AJ297356, BAA11406, BAA22231, BAB05967, C69652, CAA00273, CAA00274, CAA02196, CAA64621, CAB12064, CAB12664, CAB51971, CAB92662, CAB95850, D78508, E01340, E01903, E02083, E05047, JW0068, M74010, P37957, S23934, U78785, X95309, Z99105, and Z99108, wherein the target nucleic acid hybridizes to the unique coding oligonucleotide with at least about a 2x higher signal to noise ratio as compared to hybridization of the control nucleic acid to the coding oligonucleotide.

138. A database comprising one or more character strings corresponding to a polynucleotide sequence selected from SEQ ID NO: 1 to SEQ ID NO: 54 or a polypeptide sequence selected from SEQ ID NO: 55 to SEQ ID NO: 108.

5 **139.** The database of claim 138, wherein the one or more character strings is recorded in a computer readable medium.

140. The database of claim 139, wherein the computer readable medium comprises a medium that resides internal or external to a computer.

141. A method for manipulating a sequence record in a computer system, the method comprising:

- 10 (a) reading a character string corresponding to a polynucleotide sequence selected from SEQ ID NO: 1 to SEQ ID NO: 54 or a polypeptide sequence selected from SEQ ID NO: 55 to SEQ ID NO: 108 or a subsequence thereof;
- (b) performing an operation on the character string; and,
- 15 (c) returning a result of the operation.

142. The method of claim 141, comprising reading a character string selected by a user.

143. The method of claim 142, wherein the user selects the character string from a database or inputs the character string into the computer system.

20 **144.** The method of claim 141, comprising transmitting the selected character string to an output device.

145. The method of claim 141, comprising performing one or more operations selected from among: a local sequence comparison, a sequence alignment, a sequence identity or similarity search, a structural similarity search, a sequence identity or similarity determination, a structure determination, a nucleic acid motif determination, an amino acid

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motif determination, a hypothetical translation, a determination of a restriction map, a sequence recombination, or a BLAST determination.

146. The method of claim 145, comprising aligning the selected character string with one or more additional character strings corresponding to a polynucleotide or polypeptide sequence.

147. The method of claim 145, comprising translating one or more character strings selected from SEQ ID NO: 1 to SEQ ID NO: 54, into a character string corresponding to an amino acid sequence or translating a character string selected from SEQ ID NO: 55 to SEQ ID NO: 108, into a character string corresponding to a polynucleotide sequence.

148. The method of claim 145, comprising determining sequence identity or similarity between the selected character string and one or more additional character strings, by evaluating codon usage.

149. The method of claim 148, comprising determining optimal codon usage.

150. The method of claim 141, comprising obtaining the result of the operation on a user output device.

151. The method of claim 150, wherein the user output device is selected from among: a display monitor, a printer, and an audio-output.

152. The method of claim 141, wherein the operation comprises transmitting the character string to a device capable of producing a physical embodiment of the character string.

153. The method of claim 152, comprising obtaining the result by obtaining a nucleic acid corresponding to the character string.

154. The method of claim 152, comprising obtaining the result by obtaining a polypeptide or peptide corresponding to the character string or a sub-portion thereof.

155. The method of claim 152, wherein the device comprises an oligonucleotide synthesizer.

156. The method of claim 152, wherein the device comprises a peptide synthesizer.

157. A method of producing a modified or recombinant nucleic acid comprising mutating or recombining a nucleic acid of claim 88 or 89.

158. A modified or recombinant nucleic acid produced by the method of claim 157.

5 **159.** The method of claim 157, comprising recursively recombining the nucleic acid with one or more additional nucleic acids.

160. A modified or recombinant nucleic acid produced by the method of claim 159.

10 **161.** The method of claim 159, wherein the one or more additional nucleic acids encode a polypeptide comprising lipase activity or an amino acid subsequence or fragment thereof.

162. The method of claim 159, wherein the recursive recombination is performed in vitro.

15 **163.** The method of claim 159, wherein the recursive recombination is performed in vivo.

164. The method of claim 159, wherein the recursive recombination produces at least one library of recombinant nucleic acids, which library comprises at least one polypeptide comprising lipase activity, or a homologue thereof.

165. A nucleic acid library produced by the method of claim 164.

20 **166.** A population of cells comprising the library of claim 165.

167. The modified or recombinant nucleic acid produced by the method of claim 157.

168. A cell comprising the nucleic acid of claim 167.

25 **169.** A method of producing a polypeptide, the method comprising: (a) introducing a nucleic acid of claim 88, 89, or 112, into a population of cells, which nucleic acid is operably linked to a regulatory sequence capable of directing expression of a polypeptide encoded by the nucleic acid in at least a subset of the population of cells or progeny thereof; and, (b) expressing the polypeptide in at least the subset of the population of cells or progeny thereof.

30 **170.** The method of claim 169, further comprising isolating the polypeptide from the cells.

171. The method of claim 169, comprising expressing the polypeptide by culturing the population or subset of the population of cells in a nutrient medium under conditions in which the regulatory sequence directs expression of the polypeptide encoded by the nucleic acid.

5 172. The method of claim 169, further comprising isolating or recovering the polypeptide from the cells or from the nutrient medium.

173. The method of claim 169, wherein the culturing is performed in a bulk fermentation vessel.

174. The method of claim 169, wherein the cells are bacterial cells.

10 175. The method of claim 169, wherein the cells are eukaryotic cells.

176. The method of claim 175, wherein the cells are fungal cells, yeast cells, plant cells, insect cells, or mammalian cells.

15 177. The method of claim 176, wherein the mammalian cells comprise fertilized oocytes, embryonic stem cells, or pluripotent stem cells, further comprising regenerating a transgenic mammal expressing the polypeptide, and recovering the polypeptide from the transgenic mammal or a by-product of the transgenic animal.

178. The method of claim 177, wherein the by-product is milk.

179. A polypeptide produced by the method of claim 169.

20 180. A method of hydrolyzing a lipid to therapeutically or prophylactically treat a gastrointestinal lipid related condition/disease/disorder, the method comprising: expressing in a target cell or contacting a target cell with an effective amount of a polypeptide of claim 1 or 47.